

AMENDMENTS TO THE CLAIMS:

Please amend the claims as shown below. A complete listing of the claims, including their current status identifier, is set forth below.

1. (Currently amended) A method of identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell, the method comprising

(i) identifying a set of regions of genomic DNA to which the protein of interest is bound in the cell;

(ii) identifying candidate DNA-binding sites in the identified regions of genomic DNA, wherein a candidate DNA-binding site comprises a sequence corresponding to a DNA-sequence motif for the protein of interest, **and wherein said DNA sequence motif is enriched in said identified regions by a statistically significant amount relative to a set of genomic regions which are bound by a mutant form of the protein of interest in the cell;**

(iii) determining if the candidate DNA-binding sites are conserved in an equivalent genomic region in one or more species different from the species from which the cell is obtained, wherein a candidate DNA-binding site that is conserved in at least one of the different species is a biologically-active DNA-binding site.

2-7. (Cancelled)

8. (Original) The method of claim 1, wherein the regions of genomic DNA comprise promoter regions.

9- 11. (Canceled)

12. (Currently amended) The method of **claim 1** ~~claim 2~~, wherein a candidate DNA-binding site is conserved if the equivalent genomic region in at least one different species comprises a nucleic acid sequence that matches the DNA-sequence motif for the protein of interest.

13- 15. (Canceled)

16. (Previously presented) The method of claim 1, wherein the candidate DNA-binding site is less than 20 bp in length.

17. (Original) The method of claim 1, wherein the DNA-sequence motif is degenerate in at least one position.

18. (Canceled)

19. (Original) The method of claim 1, wherein step (iii) comprises determining if the candidate DNA-binding sites are conserved in equivalent genomic regions in two or more different species.

20-23. (Canceled)

24. (Original) The method of claim 1, wherein the set of biologically-active DNA-binding sites comprises one or more biologically-active DNA-binding sites.

25. (Canceled)

26. (Original) The method of claim 1, wherein two regions of genomic DNA are equivalent if they both comprise a sequence of at least one orthologous gene.

27. (Canceled)

28. (Original) The method of claim 1, wherein the cell is an eukaryotic cell.

29-35. (Canceled)

36. (Currently amended) A method of identifying an agent which alters the set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell, the method comprising
(i) contacting an experimental cell with a candidate agent;

(ii) identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of the cell of step (i) ~~by: according to the method of claim 2;~~

(a) identifying a set of regions of genomic DNA to which the protein of interest is bound in the cell;

(b) identifying candidate DNA-binding sites in the identified regions of genomic DNA, wherein a candidate DNA-binding site comprises a sequence corresponding to a DNA-sequence motif for the protein of interest, wherein the DNA sequence motif is enriched by a statistically significant amount relative to a suitable control;

(c) determining if the candidate DNA-binding sites are conserved in an equivalent genomic region in one or more species different from the species from which the cell is obtained, wherein a candidate DNA-binding site that is conserved in at least one of the different species is a biologically-active DNA-binding site;

thereby generating an experimental set of biologically-active DNA-binding sites;

(iii) comparing

(1) the experimental set of biologically-active DNA-binding sites to

(2) a control set of biologically-active DNA-binding sites for the protein of interest;

wherein a candidate agent is identified if the experimental set and the control set differ.

37. (Canceled)

38. (Original) A method of identifying a pathway that is transcriptionally regulated by a protein of interest in a cell, the method comprising

(i) identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of the cell according to the method of claim 1; and

(ii) identifying at least two candidate genes likely to be regulated by binding of the protein of interest to the set of biologically-active DNA-binding sites identified in (i); wherein a pathway that is transcriptionally regulated by the protein of interest is identified if at least two candidate genes are members of the same pathway.

39-40. (Canceled)

41. (Original) The method of claim 38, wherein the pathway is a gene expression pathway.

42-44. (Canceled)

45. (Currently amended) A method of identifying two sets of conditions in which a protein of interest differentially binds to the genome of a cell, the method comprising:

(i) identifying, according to the method of claim 1,

(1) a first set of biologically-active DNA-binding sites for the protein of interest in the genome of a cell, wherein the cell is exposed to a first set of conditions; and

(2) identifying a second set of biologically-active DNA-binding sites for the protein of interest in the genome of a cell, wherein the cell is exposed to a second set of conditions; and

(ii) ~~(iii)~~ identifying a difference in ~~comparing~~ the first set of biologically-active DNA-binding sites **relative to** the second set of biologically-active DNA-binding sites, **thereby identifying two sets of conditions in which a protein of interest differentially binds to the genome of a cell** ~~and determining if the two sets differ.~~

46. (Currently amended) A method of identifying a property of a gene product of a gene of interest that correlates with the binding activity of a polypeptide encoded by the gene of interest to the genome of a cell, the method comprising

(i) identifying two sets of conditions in which a protein of interest differentially binds to the genome of the cell according to the method of claim 45;

(ii) determining a property of a gene product of the gene of interest in (a) a cell exposed to the first set of conditions; and in (b) a cell exposed to the second set of conditions; and

(iii) determining if at least one property of the gene product differs in the two cells of step (ii), thereby identifying a property **of said gene product** that correlates with the binding activity of a **said polypeptide** ~~gene of interest~~ to the genome of a cell.

47. (Original) A method of identifying a property of a gene product of a gene of interest that correlates with the binding activity of a polypeptide encoded by the gene of interest to the genome of a cell, the method comprising

(i) identifying an agent which alters the set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell according to the method of claim 36;

(ii) determining a property of a gene product of the gene of interest in (a) a cell contacted with the agent; and in (b) a cell not contacted with the agent; and

(iii) determining if at least one property of the gene product differs in the two cells of step (ii), thereby identifying a property that correlates with the binding activity of a gene of interest to the genome of a cell.

48. (Previously presented) The method of claim 46, wherein the property is selected from the group consisting of a protein modification, expression level, enzymatic activity and intracellular localization.

49-59. (Canceled).

60. (Previously presented) A method of identifying two cell genotypes in which a protein of interest differentially binds to the genome, the method comprising:

(i) identifying a first set of biologically-active DNA-binding sites for the protein of interest in the genome of a cell of a first genotype;

(ii) identifying a second set of biologically-active DNA-binding sites for the protein of interest in the genome of a cell of a second genotype;

(iii) comparing the first set of biologically-active DNA-binding sites to the second set of biologically-active DNA-binding sites and determining if the two sets differ, thereby identifying two cell genotypes in which said protein of interest differentially binds to the genome.